

Score: 43.00 Marches: 43  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 5.93% Indels: 0  
 DB: Gaps: 0

US-10-735-098-2 (1-725) x BD074758 (1-2262)

Qy 171 AgleuglyTyAspGlyPheValTyTyrSerGlyGluArgProSerGlnSerLeuPro 190  
 AF072890  
 Db 526 CCTTAGTTGACGGTTGATATTCCGGAGACGTCCTCCAACTTACCG 585  
 191 SerAlaGlyThrAlaGlyTyrSerGlyAsnTrpGlnTyrMechRpaLalysAchis 2110  
 AF072890.1 G1:410392  
 586 AGTGGGGAACCGTGGAAATATCTGGTACTGGCAATAATGACCGATGCCAACGICAT 645  
 Qy 211 AzGalAlaGly 213  
 Db 646 CGAGCAGCT 654

RESULT 22

LOCUS AF072890 2519 bp DNA linear BCT 22-JAN-1999  
 DEFINITION Neisseria gonorrhoeae lactoferrin binding protein B precursor  
 ACCESSION AF072890  
 VERSION AF072890.1 G1:410392  
 KEYWORDS  
 SOURCE  
 ORGANISM Neisseria gonorrhoeae  
 Neisseria, Proteobacteria, Betaproteobacteria, Neisseriales; Neisseriaceae; Neisseria;  
 1. (bases 1 to 2519)  
 AUTHORS Biswas, G.D., Anderson, J.E., Aben, C.J., Cornelissen, C.N. and Sparling, P.F.  
 TITLE Identification and functional characterization of the Neisseria gonorrhoeae lbpB gene product  
 JOURNAL Infect. Immun. 67 (1), 455-459 (1999)  
 MEDLINE 99081783  
 PUBMED 9864256  
 REFERENCE 2 (bases 1 to 2519)  
 AUTHORS Biswas, G.D., Anderson, J.E., Cornelissen, C.N. and Sparling, P.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521 Burnett-Womack/CB 7030, Chapel Hill, N.C. 27599, USA  
 FEATURES B SOURCE  
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 184. .209  
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 /db\_xref="GI:410393"  
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 EONSGGERFRTHRGDODFVYVIGSERPSQSUSPAGTIVFPGNQWQIMDAAKHKIGKVA

RESULT 22

LOCUS AF072890 2519 bp DNA linear BCT 22-JAN-1999  
 DEFINITION Neisseria gonorrhoeae lactoferrin binding protein B precursor  
 ACCESSION AF072890  
 VERSION AF072890.1 G1:410392  
 KEYWORDS  
 SOURCE  
 ORGANISM Neisseria gonorrhoeae  
 Neisseria, Proteobacteria, Betaproteobacteria, Neisseriales; Neisseriaceae; Neisseria;  
 1. (bases 1 to 2519)  
 AUTHORS Biswas, G.D., Anderson, J.E., Aben, C.J., Cornelissen, C.N. and Sparling, P.F.  
 TITLE Identification and functional characterization of the Neisseria gonorrhoeae lbpB gene product  
 JOURNAL Infect. Immun. 67 (1), 455-459 (1999)  
 MEDLINE 99081783  
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 REFERENCE 2 (bases 1 to 2519)  
 AUTHORS Biswas, G.D., Anderson, J.E., Cornelissen, C.N. and Sparling, P.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521 Burnett-Womack/CB 7030, Chapel Hill, N.C. 27599, USA  
 FEATURES B SOURCE  
 1. 2.519  
 /organism="Neisseria gonorrhoeae"  
 /mol\_type="genomic DNA"  
 /strain="FA19"  
 /db\_xref="taxon:485"  
 184. .209  
 /note="putative"  
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 DFLFLYKOSKGKLUQQLKSEIHKRDSDVIRTEKRNKCYGFVDFGCVYVYKGBI  
 EONSGGERFRTHRGDODFVYVIGSERPSQSUSPAGTIVFPGNQWQIMDAAKHKIGKVA

ORIGIN

Alignment Scores:

Pred. No.: 9.228-35 Length: 2519  
 Score: 41.00 Matches: 41  
 Percent Similarity: 100.00% Conservative: 0  
 Best local Similarity: 100.00% Mismatches: 0  
 Query Match: 5.66% Indels: 0  
 DB: Gaps: 0

US-10-735-098-2 (1-725) x AF072890 (1-2519)

Qy 101 GluGlyAspValLeuPheLeuTyGlySerGlyAsnLysLeuGlnGlnLeuYser 120  
 AF072890  
 Db 610 GAGGGTGATGTTCTGTTTATACGGTCAAAGAAATTAACTTCACAACTTAAGC 669  
 121 GluLeuHisLysValAspSerAspValGlyLeuGlySerGlyLysGluAsnLysLys 140  
 Db 670 GAAATTCAAAACGGATTCGATGATGAAATTAGGACCTGAGAAAGGAAATTAAGA 729  
 Qy 141 Tyr 141  
 Db 730 TAT 732

RESULT 23

LOCUS NGU16260 3300 bp DNA linear BCT 27-FEB-1996  
 DEFINITION Neisseria gonorrhoeae lactoferrin receptor precursor (lbpA) gene, complete cds.  
 ACCESSION U16260  
 VERSION U16260.1 G1:915277  
 KEYWORDS  
 SOURCE  
 ORGANISM Neisseria gonorrhoeae  
 Neisseria, Proteobacteria, Betaproteobacteria, Neisseriales; Neisseriaceae; Neisseria;  
 1. (bases 1 to 3300)  
 AUTHORS Biswas, G.D. and Sparling, P.F.  
 TITLE Characterization of lbpA, the structural gene for a lactoferrin receptor in Neisseria gonorrhoeae  
 JOURNAL Infect. Immun. 63 (8), 2558-2567 (1995)  
 MEDLINE 95347808  
 PUBMED 7622218  
 REFERENCE 2 (bases 1 to 3300)  
 AUTHORS Biswas, G.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-OCT-1994) Gour D. Biswas, Dept. of Medicine/Div. of Infect. Dis., University of North Carolina, 521 Burnett-Womack  
 CB#7030, Chapel Hill, NC 2759-7030, USA  
 FEATURES B SOURCE  
 1. .3300  
 /organism="Neisseria gonorrhoeae"  
 /mol\_type="genomic DNA"  
 /strain="FA19"  
 /specific\_host="Homo sapiens"



US-10-735-098-2 (1-725) X AAX26577 (1-2058)

lment Scores:	0.0171	Length:	2040	Qy
No.:	13.00	Matches:	13	
e:	100.00%	Conservative:	0	
ent Similarity:	100.00%	Minmatch:	0	
		Db	1900	ggggTTTACGSCCTAAAGCCAGAGTGGCGGA 1938

Match: 1.79% Index Gaps

649 GLYGLYPheTyrglyProlySalaGluGluLeuGlyGly 661  
 1882 GGCCTGTTTACGGGCCTAAAGCCGAGATTGGGGGG 1920

JLT 19  
;6577  
AXX26577 standard; DNA; 2058 BP.

AAX26577;  
14-JUN-1999 (first entry)

TpB coding sequence from *Neisseria meningitidis* strain 8680  
Low molecular weight subunit; TpB; human transferrin receptor  
*Neisseria meningitidis*; vaccine; meningococcal infection; mea-

**Key**      Location/Qualifiers  
**Neisseria meningitidis.**

	CDS
sig_peptide	1. 2058 /*tag= a
mat_peptide	1. 48 /*tag= b
	49 2058

WO9907741-A1.  
mat\_peptide /\*tag= C

18-FEB-1999.  
03-AUG-1998; 98WO-FR001730

07-AUG-1997; 9/FR-00010301.  
(INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.  
Guenther-Miller M. Rokbi B:

WPT; 1999-190036/16.  
P-PSDB; AAY011525.

Vaccine containing small subunit or heat-killed *Neisseria meningitidis* - for treatment  
Disclosure: Page 40-43; 73pp; French.

The present sequence encodes the low molecular weight subunit (TbpB) of the human transferrin receptor (hTfR) from a specific strain of *Neisseria meningitidis* that contains TbpB-encoding DNA. Compositions containing TbpB are used as vaccines for treatment or prevention of meningococcal

infections, particularly meningitis  
Sequence 2058 BP; 621 A; 477 C; 551 G; 409 T; 0 U; 0 Other;

Alignment Scores:  
-ed. No.: 0.0172  
core: 13.00  
recent Similarity: 100.00%  
1st Local Similarity: 100.00%  
every Match: 1.79%  
gap: 2  
Length: 1  
Matches: 1  
Conservative: 1  
Mismatches: 1  
Indels: 1  
Gaps: 1

Willet  
9.1



Iron uptake protein; transferrin binding protein; TbpA; TbpB; vaccine; non-infectious disease; meningococcal disease; gonococcal disease; anti-inflammatory; antibacterial; ds.

Neisseria meningitidis.

Key

CDS

Location/Qualifiers

1. .2139

/\*tag= a

/product= "Neisseria meningitidis TbpB protein"

W020073080-A2.

04-OCT-2001.

27-MAR-2001; 200004-GB001348.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Gorringe AR, Hudson MJ, Matheson MA, Robinson A, West DM;

WPI; 2001-616522/71.

P-PSDB; AAE12019.

Non-neisserial cells useful in manufacturing of vaccines without the loss of antigenicity of the native protein, against meningococcal diseases such as meningitis, express a recombinant non-neisserial iron uptake protein.

Example 1: Page 19-21; 57pp; English.

The present invention relates to a non-neisserial cell expressing a non-neisserial iron uptake protein, where non-neisserial iron uptake proteins including transferrin binding protein (Tbp) A and TbpB can be extracted from the cell under mild conditions and retains substantially the antigenicity of native iron uptake protein. The non-neisserial cell is useful in manufacture of Tbp, and in the manufacture of vaccines for protection against native non-neisserial disease, meningococcal disease and/or gonococcal disease. The affinity matrix is useful for purifying a Tbp, where Tbp containing a preparation is eluted through the matrix. The present sequence is a Neisseria meningitidis strain K454 tpbB gene

Sequence 2139 BP; 696 A; 492 C; 519 G; 432 T; 0 U; 0 Other; Alignment Scores: Pred. No.: 0.0179 Length: 2139

sd. No.: 13.00 Matches: 13

ore: 100.00% Conservative: 0

cent Similarity: 100.00% Mismatches: 0

st Local Similarity: 100.00% Indels: 0

ry Match: 1.79% Gaps: 0

5

-10-735-098-2 (1-725) x AA019530 (1-2139)

649 GlyGlyPheTyrglyProlysAlaGluGluGlyGly 661  
1993 GGCCTTTACGGCCCAAAGCCGAAGAGTTGGCGGA 2031

JULT 26 AAQ55619 standard; DNA; 2230 BP.

AAQ55619; 16-OCT-2003 (revised)  
25-MAR-2003 (revised)  
15-JUL-1994 (first entry)

N.meningitidis IM2169 transferrin receptor Tbp2 subunit DNA sequence.  
Transferrin receptor; Tbp2 subunit; strain IM2169; meningitis vaccine;

Iron transport protein; iron chelator; ss.  
Neisseria meningitidis; (strain IM2169).  
Key  
CDS  
Location/Qualifiers  
/\*tag= a  
/\*tag= b  
/\*tag= C  
/product= "Tbp2"  
/product= "Tbp2"  
FR2692592-A1  
24-DEC-1993.  
19-JUN-1992; 92FR-00007493.  
(INMR ) PASTEUR MERLEUX SERUMS & VACCINS.  
(TRGE ) TRANSGENE SA.  
Jacobs E, Legrain M, Mazarin V, Bouchon-Rheisen B, Shryvers AB;  
Bloch M;  
DR WPI; 1994-028254/04.  
P-PSDB; AAR48222.

P-PSDB; AAE12019.

PT DNA coding for neisseria meningitidis proteins - namely transferrin receptor subunits.

PT

PS Claim 2-7 and 11-12; Page 36-40; 60pp; French.

CC Sequences coding for the Tbp1 and Tbp2 transferrin receptor subunits were isolated from a Neisseria meningitidis strain IM2169 genomic DNA library (see AAQ55618 and AAQ55619, respectively). Cells transformed with the DNA can be used for large scale production of the receptor proteins. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 2230 BP; 727 A; 483 C; 547 G; 473 T; 0 U; 0 Other;

Alignment Scores: Pred. No.: 0.0186 Length: 2230

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.79% Indels: 0

DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AAQ55619 (1-2230)

Qy 649 GlyGlyPheTyrglyProlysAlaGluGluGlyGly 661  
Db 2037 GGGGTTTACGGCCCAAAGCCGAAGAGTTGGCGGA 2075

RESULT 27

ART11238 ID ART11238 standard; DNA; 2230 BP.

XX AC ART11238;

XX DR 16-OCT-2003 (revised)  
30-AUG-1996 (first entry)

XX DE Neisseria meningitidis strain IM2169 transferrin receptor Tbp2 gene.

XX KW Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine; passive immunisation; immunotherapy; ss.

XX OS Neisseria meningitidis; (strain IM2169).

DOKRYSSTKRASSSWSTADVSAYNLKKRRTLRAAIYNIGNYRYVTWESLRQTAESTAN  
RHCDDSNYGRYAAPCRNESTIALEMKE"

**ORIGIN** DOKRYSTKRASSNMSTADSYALNKKRITLRAAYNINGRYVWESRQTAESTAN  
**Alignment Scores:** RHHGDSNYGRYAAPGRNFSLALEMKF"  
**Pred. No.:** 4 3e-186 **Length:** 3398  
**Score:** 183.00 **Matches:** 183  
**Percent Similarity:** 100.00% **Conservative:** 0  
**Best Local Similarity:** 100.00% **Mismatches:** 0  
**Query Match:** 24.70% **Indels:** 0  
**DB:** 1 **Gaps:** 0  
**US-10-735-098-6 (1-741) X NMTRBAC (1-3398)**

REFERENCE	AUTHORS	LOCUS	DEFINITION	VERSION	ACCESSION	KEYWORDS	ORGANISM	RESCDFT
1	Petterson, A., Klarenbeek, V., van Deurzen, J., Poolman, J.T. and Tommassen, J.	N meningitidis (H44/76) lbpA gene.	lactoferrin binding protein, lbpA gene.	X79838	X79838_1	GI:503053	N meningitidis	NMLBPA
2	Petterson, A., Klarenbeek, V., van Deurzen, J., Poolman, J.T. and Tommassen, J.	Molecular characterization of the structural gene for the lactoferrin receptor of the meningococcal strain H44/76	lactoferrin receptor of the meningococcal strain H44/76	95272374	95272374	Pubmed: 7752881	Bacterium; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.	LOCUS
3	Petterson, A.M.	Submitted (23-JUN-1994)	Direct Submission	1	1	3398	Utrecht University, Padualaan 8, 3584 CH Utrecht, NETHERLANDS	DEFINITION
4	Petterson, A.M.	A.M. Petterson, Dept of Mol Cell Biology, Location/Qualifiers		2	2	(bases 1 to 3398)		VERSION
5	Petterson, A.M.	1		3398	3398			ACCESSION
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8		/strain="H44/76"						RESCDFT
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21		/protein_id="CAN56233_1"						
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23		/db_xref="GO:051187"						
24		/db_xref="UniProt/TREMBL:051187"						
25		/translation="MNKHSFPLTLTALATAPPSVANSEPTAQTOSKEVTYRAA						
26		KVGRRSKEVTGKGKIVKETSTLNKEQVQIQLDTRPQVAVGKSGGIVSRV						
27		DKNRVAVSVDGVQAQIQTFTVQCSQGGSGGATBENIVISTWEIKDGGSSD						
28		GSGALGSGAVKRTKEADLISQGKSKQIAKQAYGSKNQFRQMKSLGAGSKQKGWEGIL						
29		IRTCQCGTTRPHGDTADGVEYKIDAFRQYDQKQNGKAYFLLGESEELKPA						
30		KLAGNGYKQNLNRAWEERKKNQNSAEEARVRAQARHENLSAQAYTGGCILP						
31		DPMDSYGSWMLAKLGTRFGGRYIVGKVFDTKORYJRDIMTEKQYGTDEATKFDKS						
32		GVYGDGFDRGFLYFVFTMEKQGKSKRIFDEHRRRMLGKIRKEN						
33		EAYSDWADKAVALSFDQGQVADNTTCKNCAVPSYDACKASADPSYKVSQDRH						
34		YRHOHNTLNAPEKSLKNSKWTQHHLTGFGYDQKAVSRPQLSHNAR1SPFDAD						
35		DGKYVLLKGKPVWESVYKLTGSKVPRKNSNLSNDRFSGKDFSL						
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88		YRHOHNLTEIDYRNAQNSLQNTGKIDQWMLVQGKPEGLVQGKQWGANIMTYSKRNPDALYAG						
89		YRHOHNLTEIDYRNAQNSLQNTGKIDQWMLVQGKPEGLVQGKQWGANIMTYSKRNPDALYAG						
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123		YRHOHNLTEIDYRNAQNSLQNTGKIDQWMLVQGKPEGLVQGKQWGANIMTYSKRNPDALYAG						
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149								



### Alignment Scores:

W.S.B. 89

KIDERKRPLTIYBITATLDGENRFTGSAKVNTHLKTSHADKEHLFHTTBABORLEGFFG  
DKGEELLAGRFISNDNSVFGVFAGKKTNASMAADTNPAMPSEKHTKILDSLKISWEAT

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    Score: 70.00
    Percent Similarity: 100.00%
    Best Local Similarity: 100.00%
    Query Match: 9.66%
DB: 1
Length: 33.8867
Matches: 100
Conservative: 100
Mismatches: 0
Indels: 0
Gaps: 0

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ORIGIN

Length:	2226
Matches:	57
Conservative:	0
Mismatches:	0
Indices:	0
Gaps:	0

AF123380 AF123380 2226 bp DNA linear BCT 24-MAY-1999  
 LOCUS Neisseria meningitidis strain H44/76 lactoferrin-binding protein  
 DEFINITION .precursor (lbpB) gene, complete cds.  
 ACCESSION AF123380  
 VERSION AF123380.1  
 SOURCE GI:484686

QY	41	Phel <u>Y</u> Ser <u>L</u> Asp <u>Y</u> Alp <u>Y</u> Pro <u>Y</u> Thr <u>Y</u> Pro <u>Y</u> Pro <u>Y</u> Pro <u>Y</u> Ala <u>Y</u> lys <u>Y</u> Pro <u>Y</u> Ser <u>L</u> le <u>Y</u> Glu	57
Db	121	TCAAGTCTAGGACGTTCCCACTCCGCCCCCTGCCAAACCTCTATAGAA	171
RESULT	8		
A98972			

ORGANISM	Bacteriia; Proteobactridia; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE	1 (bases 1 to 2226)
AUTHORS	Petterson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.
TITLE	Sequence variability of the meningococcal lactoferrin-binding protein lbpB
JOURNAL	Gene 231 (1-2), 105-110 (1999)
MEDLINE	99250255
PUBMED	1023154
REFERENCE	2 (bases 1 to 2226)
AUTHORS	Petterson,A., van der Biezen,J., Joosten,V., Hendriksen,J. and Tommassen,J.
TITLE	Direct Submission
JOURNAL	Submitted (26-JAN-1999) Department of Molecular Cell Biology,

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organism="Neisseria meningitidis"
/mol type="genomic DNA"
/stain="H&E"
/db_xref="taxon:487"
1. 2226
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1. 2226
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-EJEWTDNRQYGSKDKLQMLDKHORNPNVREIRSENENKKYGFEDVADGYYVTTNGD  
-GDPSEDDGVLVYQNGATSYATADREKGKPAEYTDWDFKETLTGQLQKQYVK

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Score: 43.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.93%
DB: 6

Matches: 43
Mismatches: 0
Indels: 0
Gaps: 0

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QY 171 ArgIeuGlyIyrAspGlyPheValTyrTyrSerGlyGluargProserGlnSerLeuPro 190  
 Db 526 CGCTTAAGGTTATGAGCGTTGATATAATTCGGAGAACGCTCTTCCAAACTTACCG 585  
 QY 191 SerAlaGlyThrValGluTyrSerGlyAsnTrpGlyTyrMetThrAspAlaSerGly 210  
 S86 AGTGCGGGAAAGGGTGAATATTCTGTAACGGCATATAAGGACCATGCGAACCTCAT 645

Db 646 CGAGCAGGT 654

RESULT 22  
AF072890

**LOCUS** AF072890 **DEFINITION** *Neisseria gonorrhoeae* lactoferrin binding protein B precursor  
**ACCESSION** **NP\_045581** **VERSION** 1 **LENGTH** 2519 **MW** 275.5 kDa **PROTEIN** *Neisseria gonorrhoeae* lactoferrin binding protein B precursor

VERSION AF:072890.1 GI:41063922  
 KEYWORDS .  
 SOURCE *Neisseria gonorrhoeae*  
 ORGANISM *Neisseria gonorrhoeae*  
 Bacteria, prokaryotes

REFERENCE  
1 (bases 1 to 2519)  
Biswas, G. D., Anderson, W. R., Sparling, P. F.  
TITLE  
Identification and function of the *Neisseriaceae* and *Neisseri-*

JOURNAL Infect. Immun. 67 (1),  
MEDLINE 99081783  
BTMAMER 066456

REFERENCE 2 (bases 1 to 2519)  
 AUTHORS Biswas, G.D., Anderson, J.  
 TITLE Direct Submission

FEATURES	BURNETT
Source	Womack/CB 7030, Neocaine/IB, Quiv. of N. Carolina, 5221 Location/Qualifiers
1. 2519	Burnett Location/Qualifiers

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 /strain="FL19"
 /db_xref="Taxon:485"
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/protein="2496"
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protein_bind 276. "293"
protein_bind 276. "1bpB"
protein_bind 276. "1bpR"
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/locus\_tag="Bacillus\_vulgaris\_subsp\_vulgaris\_EG400\_301\_304\_FUR"  
/bound\_motif="FUR"  
/gene="lbpB"  
310 . 2496

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/product="lactoferrin binding protein B precursor"  
/protein_id="NP_001000000.1"
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EONGGKRFTHRFGDFTYSGRPSQSLPSAGTYVKYRGMWOMDVKHTRGKA

ORIGIN	Alignment Scores:
sig_peptide	310. .363
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misc_feature	/gene="lppB" /product="lactoferrin binding protein B" 1902. .1311
	/gene="lppB" /note="encodes gonococcal uptake sequence"

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Pred. No.: 9/22e-35 Length:
Score: 41.00 Matches:
percent Similarity: 100.00% Conservatives:
Best Local Similarity: 100.00% Mismatches:
Query Match: 5.66% Indels:
DB: 1 Gaps:

```

101 GLUGIYIAspValLeuPheLeuTrGlySerLysGlyAsnLysLeuGlnGlnLeuLysSer 120  
 610 GAGGIGGATGTTCTGTTTATACGGTTAAAGGAAATAACTTCACAACTTAAGC 669  
 121 GluIleHisIysArgAspSerAspValGluIleArgThrSerGluLysGluLysIys 140  
 670 GAAATTCATAAACGTCGATTCGCTGAGTAGAAATTAGACGTCAGAAAGGAAATAAAA 729  
 QV  
 141 Tyr 141

Db 730 TAT 732  
 RESULT 23  
 NGU15260  
 FOCUS NGU15260 3300 bp DNA linear BCT 27-FEB-1991  
 DEFINITION *Neisseria gonorrhoeae* lactoferrin receptor precursor (lbpA) gene, complete cds.

VERSION U16260.1 GI:915277  
 KEYWORDS Neisseria gonorrhoeae  
 SOURCE Neisseria gonorrhoeae  
 ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria

**AUTHORS** Biswas, G.D. and Sparling, P.F.  
**TITLE** Characterization of *lbpa*, the structural gene for a lactoferrin receptor in *Neisseria gonorrhoeae*  
**JOURNAL** *Infect Immun* 53 (1985) 1000-1005

MEDLINE 95347808  
PUBMED 7622218  
REFERENCE 2 (bases 1 to 3300)

**FEATURES** Direct Submission  
TITLE Submitted (24-OCT-1994) Gour D. Biswas, 'Dept. of Medicine/Div. of  
JOURNAL Infec. Dis., University of North Carolina, 521 Burnett-Womack  
CB#7030, Chapel Hill, NC 27599-7030, USA  
LOCATION/QUALIFIERS



## nment Scores:

No.: 0.0171 Length: 2040  
 e: 13.00 Matches: 13 Conservative: 0  
 ent Similarity: 100.00% Mismatches: 0  
 Local Similarity: 1.79% Indels: 0  
 y Match: 2 Gaps: 0

0-735-098-2 (1-725) x AAX26577 (1-2040)

649 GlyGlyPheTyrGlyProlysalGluIleuGlyGly 661  
 1882 GCGGTTTACGGCTTAACCCGAGAGTGGCGGG 1920

ILT 19  
 AAX26577 standard; DNA; 2058 BP.

!6577 14-JUN-1999 (first entry)

TbpB coding sequence from *Neisseria meningitidis* strain 8680.

low molecular weight subunit; TbpB; human transferrin receptor; hTfR; *Neisseria meningitidis*; vaccine; meningococcal infection; meningitis; ss.

*Neisseria meningitidis*.

Key location/Qualifiers

CDS 1. .2058  
 sig\_peptide 1. .48  
 mat\_peptide /\*tag= c

W09907741-A1.

18-FEB-1999. 98WO-FR001730.

03-AUG-1998; 97FR-00010301.

(INMR ) PASTEUR MERIEUX SERUMS & VACCINS SA.

Quentin-Millet M, Rokbi B;

WPI: 1999-190036/16.

P-PSDB; AAY01525.

Vaccine containing small subunit of human transferrin receptor from *Neisseria meningitidis* - for treatment and prevention of meningitis.

Disclosure: Page 40-43; 73PB; French.

The present sequence encodes the low molecular weight subunit (TbpB) of the human transferrin receptor (hTR) from a specific strain of *Neisseria meningitidis* that contains TbpB-encoding DNA. Compositions containing TbpB are used as vaccines for treatment or prevention of meningococcal infections, particularly meningitis

Sequence 2058 BP; 621 A; 477 C; 551 G; 409 T; 0 U; 0 Other;

ignment Scores: 0.0172 Length: 2058  
 ed. No.: 13.00 Matches: 13 Conservative: 0  
 ore: 100.00% Mismatches: 0  
 recent Similarity: 100.00% Indels: 0  
 ist Local Similarity: 1.79% Gaps: 0  
 ery Match: 2

US-10-735-098-2 (1-725) x AAX26577 (1-2058)

QY 649 GlyGlyPheTyrGlyProlysalGluIleuGlyGly 661  
 DB 1900 GCGGTTTACGGCTTAACCCGAGAGTGGCGGG 1938

RESULT 20  
 ART11243  
 ID AAT11243 standard; DNA; 2070 BP.

XX AC AAT11243;  
 XX DT 16-OCT-2003 (revised)  
 XX DT 02-SEP-1996 (first entry)

DB Neisseria meningitidis strain B283 transferrin receptor Tbp2 gene.

XX KW Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine; passive immunisation; immunotherapy; IM2169; IM2394; ss.

XX OS Neisseria meningitidis; (strain B283).

XX Key Location/Qualifiers  
 PH 1. .2070  
 FT CDS /\*tag= a  
 FT sig\_peptide 1. .60  
 FT /\*tag= b 61. .2067  
 FT mat\_peptide /\*tag= c

FT PR 31-MAY-1994; 94FR-00006394.

XX PN W09533040-A2.  
 XX PD 07-DEC-1995.

XX PF 30-MAY-1995; 95WO-FR000701.

XX PT 31-MAY-1994; 94FR-00006394.

XX PA (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.  
 PA (TRGE ) TRANSGENE SA.

XX PI Millet MBJ, Lissolo L, Mazarin V, Legrain M, Jacobs E;  
 XX DR WPI; 1996-030562/03.  
 XX DR P-PSDB; AAR88648.

XX PT Polypeptide(s) for vaccination against *Neisseria meningitidis* group B - comprising deletion mutants of transferrin receptor Tbp2 subunit.

XX PT comprising deletion mutants of transferrin receptor Tbp2 subunit.  
 XX PS Disclosure; Page 76-81; 11app; French.

The present sequence is that of the *N meningitidis* strain B283 Tbp2 polypeptide. The Tbp2 polypeptide has three domains: an N-terminal domain, a hinge domain and a C-terminal domain; deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. The positions of the 3 domains in B283 are defined by alignment with the IM2169 sequence. The deletion mutant polypeptides of the invention can generate an immune response against *N meningitidis*. (Updated on 16-OCT-2003 to standardise CC OS field)

XX SQ Sequence 2070 BP; 617 A; 472 C; 560 G; 421 T; 0 U; 0 Other;

Alignment Scores: 0.0173 Length: 2070  
 Pred. No.: 13.00 Matches: 13 Conservative: 0  
 Score: 100.00% Mismatches: 0  
 Percent Similarity: 100.00% Indels: 0  
 Best Local Similarity: 1.79% Gaps: 0  
 Query Match: 2 DB:

Db 1936 gccggTTTTACGGCCAAAGCGAGAGTTGGCGGA 1974

RESULT 22

AT11242 AT11242 standard; DNA; 2114 BP.

AC ID AT11242;

XX RAT11242;

DT 16-OCT-2003 (revised)

XX 02-SEP-1996 (first entry)

DE Neisseria meningitidis strain S3032 transferrin receptor Tbp2 gene.

KW Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine; passive immunisation; immunotherapy; IM2169; ss.

XX OS Neisseria meningitidis; (strain S3032).

XX FH Key Location/Qualifiers

XX FT CDS 1..2100

FT mat\_peptide /\*tag= a

FT 1..2097 /\*tag= b

XX PN W09533049-A2.

XX PD 07-DEC-1995.

XX PF 30-MAY-1995; 95WO-FR0000701.

XX PR 31-MAY-1994; 94FR-00006594.

XX PA (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.

PA (TRGE ) TRANSGENE SA.

XX PT Millet MBJ, Lissolo L, Mazarin V, Legrain M, Jacobs E;

DR WPI; 1996-010562/03.

DR P-PSDB; BAR08647.

XX PT <sup>7</sup>Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tbp2 subunit.

XX PS Disclosure; Page 58-61; 114pp; French.

XX The present sequence is that of the N.meningitidis strain S3032 CC transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an N-terminal domain, a hinge domain and a C-terminal domain; deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. Strain S3032 is an IM2169-related N.meningitidis strain and the positions of the 3 domains are defined by alignment with the IM2169 sequence. The deletion mutant polypeptides of the invention, can generate an immune response against N.meningitidis. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 2114 BP; 691 A; 493 C; 509 G; 421 T; 0 U; 0 other;

Alignment Scores:

Pred. No.: 0.0177 Length: 2114

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.79% Indels: 0

DB: 2 Gaps: 0



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